Restriction Map of the RSV G Gene

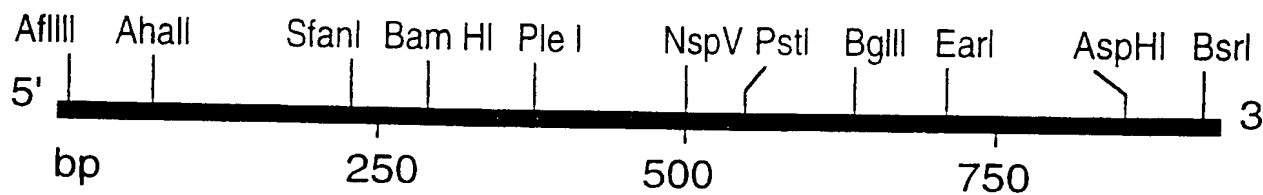AflIII   AhaII   SfanI Bam HI Ple I   NspV Pstl   Bglll   Earl   AspHI Bsrl

5'   3

bp   250   500   750

FIG.1

FIG.2A

```
        10         19        28        37        46        55
TGCAAAC ATG TCC AAA AAC AAG GAC CAA CGC ACC GCT AAG ACA CTA GAA AAG ACC
        Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Lys Thr

    64         73        82        91       100       109
TGG GAC ACT CTC AAT CAT TTA TTA TTC ATA TCA TCG GGC TTA TAT AAG TTA AAT
Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Gly Leu Tyr Lys Leu Asn

    118       127       136       145       154       163
CTT AAA TCT GTA GCA CAA ATC ACA TTA TCC ATT CTG GCA ATG ATA ATC TCA ACT
Leu Lys Ser Val Ala Gln Ile Thr Leu Ser Ile Leu Ala Met Ile Ile Ser Thr

    172       181       190       199       208       217
TCA CTT ATA ATT ACA GCC ATC ATA TTC ATA GCC TCG GCA AAC CAC AAA GTC ACA
Ser Leu Ile Ile Thr Ala Ile Ile Phe Ile Ala Ser Ala Asn His Lys Val Thr

    226       235       244       253       262       271
CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC ATC AAG AAC ACA ACC CCA
Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys Asn Thr Thr Pro

    280       289       298       307       316       325
ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TCC AAT CTG TCT GAA
Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser Asn Leu Ser Glu
```

FIG.2B

```
       334         343         352         361         370         379
ATT ACA CAA ACC ACC ATA GCT TCA ACA CCA GGA GTC AAG TCA
Ile Thr Ser Gln Thr Thr Ile Leu Ala Ser Thr Thr Pro Gly Val Lys Ser

       388         397         406         415         424         433
AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA CAA
Asn Leu Gln Pro Thr Thr Val Lys Thr Lys Asn Thr Thr Gln Thr Gln

       442         451         460         469         478         487
CCC AAG CCC ACT ACA AAA CAA CGC CAA AAC AAA CCA CCC AAT
Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn

       496         505         514         523         532         541
AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTA CCC TGC AGC AAC
Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser Asn

       550         559         568         577         586         595
AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA AAG
Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys Pro Gly Lys

       604         613         622         631         640         649
AAA ACC ACC ACC AAG CCT ACA AAA CCA ACC TTC AAG ACA ACC AAA AAA GAT
Lys Thr Thr Thr Lys Pro Thr Lys Pro Thr Phe Lys Thr Thr Lys Lys Asp
```

FIG.2C

```
      658      667      676      685      694      703
      CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC AAG CCC ACA GAA
      Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr Lys Pro Thr Glu

      712      721      730      739      748      757
      GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC ATC ACA ACT ACA CTG CTC ACC AAC
      Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr Thr Leu Leu Thr Asn

      766      775      784      793      802      811
      AAC ACA ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC TTC CAC TCA ACC
      Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr

      820      829      838      847      856      865
      TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA TCC GAG CAC CCA
      Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro

      874      883      892      901      914
      TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAGTTATTAA AAAAAAAA
      Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln  .
```

FIG.3A

```
CAC AAA GTC ACA CTA ACA ACT GCA ATA CAA GAT GCA ACA AGC CAG ATC AAG    54
His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys    18

AAC ACA ACC CCA ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TCC    108
Asn Thr Thr Pro Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser    36

AAT CTG TCT GAA ATT ACA TCA CAA ACC ATA CTA GCT TCA ACA ACA CCA    162
Asn Leu Ser Glu Ile Thr Ser Gln Thr Ile Leu Ala Ser Thr Thr Pro    54

GGA GTC AAG TCA AAC CTG CAA CCC ACA GTC AAG ACT AAA AAC ACA ACA    216
Gly Val Lys Ser Asn Leu Gln Pro Thr Val Lys Thr Lys Asn Thr Thr    72

ACC CAA ACA CAA CCC AGC AAG CCC CAA AAA CAA CGC CAA CCA CCA    270
Thr Gln Thr Gln Pro Ser Lys Pro Thr Lys Gln Arg Gln Asn Lys Pro Pro    90

AAC AAA CCC AAT AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTA CCC TGC AGC    324
Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser    108

ATA TGC AGC AAC AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA    378
Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys    126

AAA CCA GGA AAG AAA ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA    432
Lys Pro Gly Lys Lys Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys Thr    144
```

FIG.3B

```
ACC AAA AAA GAT CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC  486
Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr  162

AAG CCC ACA GAA GAG CCA ACC ATC AAC ACC AAA ACA AAC ATC ACA ACT ACA      540
Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr      180

CTG CTC ACC AAC ACC ACA GGA AAT CCA AAA CTC ACA CAA ATG GAA ACC          594
Leu Leu Thr Asn Asn Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr      198

TTC CAC TCA ACC TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA  648
Phe His Ser Thr Ser Ser Glu Gly Asn Leu Ser Gln Val Ser Thr Thr          216

TCC GAG CAC CCA TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAG      699
Ser Glu His Pro Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln          232

TTATTAA AAAAAAAA
```

FIG.4.

8/19

Eco RI
Bam HI

RSV G

pRSV G12
4130 bp

Eco RI

pCMV

Intron A

VR 1020
5100 bp

TPAsig

Bam HI

BGHpA

Bgl II

Eco RI
Klenow
Bam HI

Bgl II
Klenow
Bam HI

5' GATCCACTCAG 3' ——Ligate
    GTGAGTCCTAG

pCMV

pXL6
5734 bp

Intron A

TPA sig

RSV G

BGHpA

FIG.5

FIG.6A

```
        10         20         30         40         50         60         70
TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT

        80         90        100        110        120        130        140
GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGGGCGGTG TTGGCGGGTC TCGGGGCTTG

       150        160        170        180        190        200        210
CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA CCCGCACAGAT

       220        230        240        250        260        270        280
GCGTAAGGAG AAAATACCGC ATCAGATTGG CTATTGGCCA TTGCATACGT TGTATCCATA TCATATAATG

       290        300        310        320        330        340        350
TACATTTATA TTGCCTCATG TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT

       360        370        380        390        400        410        420
AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA CGGTAAATGG

       430        440        450        460        470        480        490
CCCGCCTGGC TGACCGCCCA ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG

       500        510        520        530        540        550        560
CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC TGCCCACTTG GCAGTACATC
```
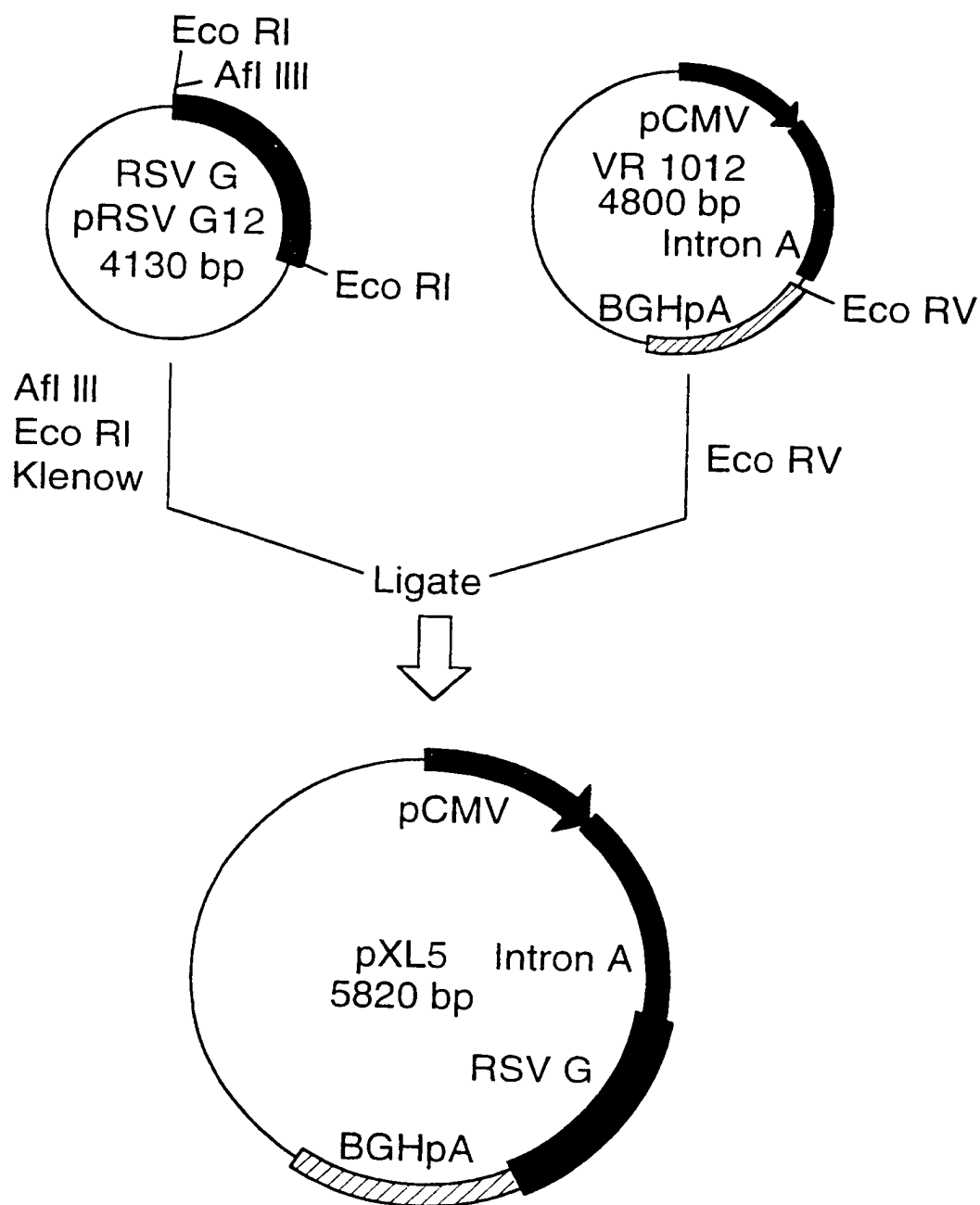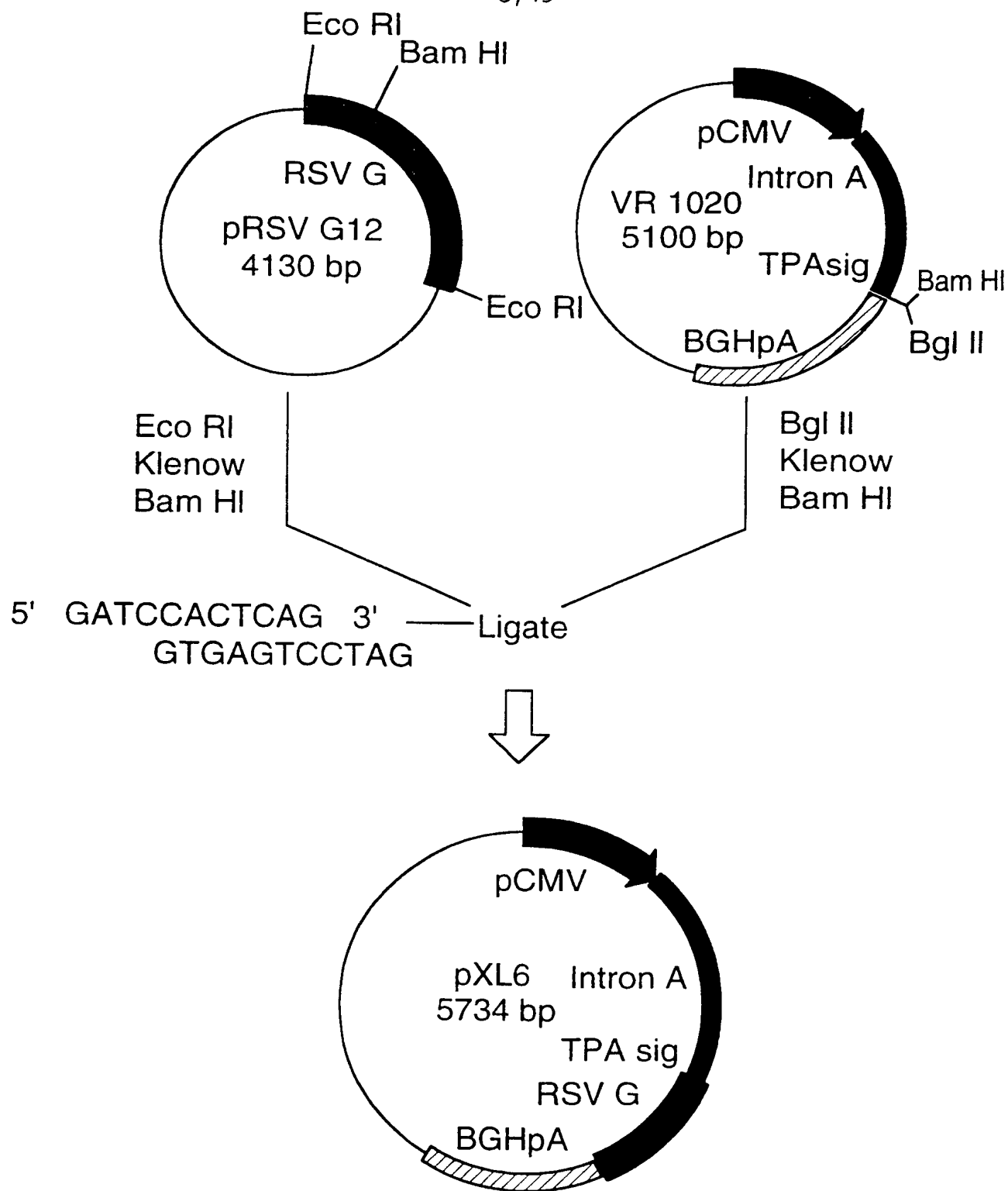
FIG.6B

```
       570        580        590        600        610        620        630
AAGTGTATCA TATGCCAAGT ACGCCCCTA TTGAGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC

       640        650        660        670        680        690        700
CCAGTACATG ACCTTATGGG ACTTTCCTAC TTGGCAGTAC AATCTACGTAT TAGTCATCGC TATTACCATG

       710        720        730        740        750        760        770
GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC GGTTTGACTC ACGGGGATTT CCAAGTCTCC

       780        790        800        810        820        830        840
ACCCCATTGA CGTCAATGGG AGTTTGTTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA

       850        860        870        880        890        900        910
CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG AGCTGTTTA

       920        930        940        950        960        970        980
GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT TTGACCTCCA TAGAAGACAC CGGGACCGAT

       990        1000       1010       1020       1030       1040       1050
CCAGCCTCCG CGGCCGGGAA CGGTGCATTG GAACGCGGAT TCCCCGTGCC AAGAGTGACG TAAGTACCGC

       1060       1070       1080       1090       1100       1110       1120
CTATAGACTC TATAGGCACA CCCCTTTGGC TCTTATGCAT GCTATACTGT TTTTGGCTTG GGGCCTATAC
```

FIG.6C

```
1130       1140       1150       1160       1170       1180       1190
ACCCCGCTT CCTTATGCTA TAGGTGATGG TATTAGCTTAG CCTATAGGTG TGGGTTATTG ACCATTATTG

1200       1210       1220       1230       1240       1250       1260
ACCACTCCCC TATTGGTGAC GATACTTTCC ATTACTAAATC CATAACATGG CTCTTTGCCA CAACTATCTC

1270       1280       1290       1300       1310       1320       1330
TATTGGCTAT ATGCCAATAC TCTGTCCTTC AGAGACTGAC ACGGACTCTG TATTTTTACA GGATGGGGTC

1340       1350       1360       1370       1380       1390       1400
CCATTTATTA TTTACAAATT CACATATACA ACAACGCCGT CCCCGTGCC CGCAGTTTTT ATTAAACATA

1410       1420       1430       1440       1450       1460       1470
GGGTGGGATC TCCACGGGAA TCTCGGGTAC GTGTTCGGA CATGGCTCT TCTCGGGTAG CGGGGGAGCT

1480       1490       1500       1510       1520       1530       1540
TCCACATCCG AGCCCTTGGTC CCATGCCTCC AGGGCCTCAT GGTCGCTCG CAGTCCTTG CTCCTAACAG

1550       1560       1570       1580       1590       1600       1610
TGGAGGCCAG ACTTAGCGCAC CCACCACCAC AGCACAAATGC CAGTGTGCCG CACAAGGCCG TGCGGGTAGG

1620       1630       1640       1650       1660       1670       1680
GTATGTGTCT GAAAAATGAGC GTGCAGATTG GGCTCGCACG GCTTGAGCGCAG ATGGAAGACT TAAGGCAGCG
```

FIG.6D

```
1690        1700        1710        1720        1730        1740        1750
GCAGAAGAAG  ATGCAGGCAG  CTGAGTTGTT  GTATTCTGAT  AAGAGTCAGA  GGTAACTCCC  GTTGCGGTGC

1760        1770        1780        1790        1800        1810        1820
TGTTAACGGT  GGAGGCCAGT  GTAGTCTGAG  CAGTACTCGT  TGCTGCCCG   CCCGCCACCA  GACATAATAG

1830        1840        1850        1860        1870        1880        1890
CTGACAGACT  AACAGACTGT  TCCTTTCCAT  GGGTCTTTTC  TGCAGTCACC  GTCGTCGACA  CGTGTGATCA

1900        1910        1920        1930        1940        1950        1960
GATATGCCGG  CCGCTCTAGA  CCAGGGGCCT  GGATCCAGAT  CTGCTGTGCC  TTCTAGTTGC  CAGCCATCTG

1970        1980        1990        2000        2010        2020        2030
TTGTTTGCCC  CTCCCCGTG   CCTTCCTTGA  CCCTGGAAGG  TGCCACTCCC  ACTGTCCTTT  CCTAATAAAA

2040        2050        2060        2070        2080        2090        2100
TGAGGAAATT  GCATCGCATT  GTCTGAGTAG  GTGTCATTCT  ATTCTGGGG   GTGGGGTGGG  GCAGGACAGC

2110        2120        2130        2140        2150        2160        2170
AAGGGGGAGG  ATTGGGAAGA  CAATAGCAGG  CATGCTCGGG  ATGGGGTGGG  CTCTATGGT   ACCCAGGTGC

2180        2190        2200        2210        2220        2230        2240
TGAAGAATTG  ACCCGGTTCC  TCCTGGGCCA  GAAAGAAGCA  GGCACATCCC  CTTCTCTGTG  ACACACCCTG
```

FIG.6E

```
      2250        2260        2270        2280        2290        2300        2310
  TCCAGCCCC  TGGTTCTTAG  TTCCAGCCCC  ACTTCATAGGA  CACTTCATAGC  TCAGGAGGGC  TCGGCCTTCA

      2320        2330        2340        2350        2360        2370        2380
  ATCCCACCCG  CTAAAGTACT  TGGAGCGGTC  TCTCCCTCCC  TCATCAGCCC  ACCAAACCAA  ACCTAGCCTC

      2390        2400        2410        2420        2430        2440        2450
  CAAGAGTGGG  AAGAAATTAA  AGCAAGATAG  GCTATTAAGT  GCAGAGGGAG  AGAAAATCCC  TCCAACATGT

      2460        2470        2480        2490        2500        2510        2520
  GAGGAAGTAA  TGAGAGAAAT  CATAGAATTT  CTTCCCGCTTC  CTCGCTCACT  GACTCGCTGC  GCTCGGTTGT

      2530        2540        2550        2560        2570        2580        2590
  TCGGCTGCGG  CGAGCGGTAT  CAGCTCACTC  AAAGGCGGTA  ATACGGTTAT  CCACAGAATC  AGGGGATAAC

      2600        2610        2620        2630        2640        2650        2660
  GCAGGAAAGA  ACATGTGAGC  AAAAGGCCAG  CAAAAGGCCA  GGAACCGTAA  AAAGGCCGCG  TTGCTGGCGT

      2670        2680        2690        2700        2710        2720        2730
  TTTTCCATAG  GCTCCGCCCC  CCTGACGAGC  ATCACAAAAA  TCGACGCTCA  AGTCAGAGGT  GGCGAAACCC

      2740        2750        2760        2770        2780        2790        2800
  GACAGGACTA  TAAAGATACC  AGGCGTTTCC  CCCTGGAAGC  TCCCTCGTGC  GCTCTCCTGT  TCCGACCCTG
```

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PCT/CA98/00697

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FIG.6F

```
     2810       2820       2830       2840       2850       2860       2870
COGCTTACCG GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA

     2880       2890       2900       2910       2920       2930       2940
GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA

     2950       2960       2970       2980       2990       3000       3010
CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA

     3020       3030       3040       3050       3060       3070       3080
GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC

     3090       3100       3110       3120       3130       3140       3150
CTAACTACGG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA

     3160       3170       3180       3190       3200       3210       3220
AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG

     3230       3240       3250       3260       3270       3280       3290
CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT

     3300       3310       3320       3330       3340       3350       3360
GGAACGAAAA CTGACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT
```

FIG.6G

```
3370       3380       3390       3400       3410       3420       3430
AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TTACCAATGC

3440       3450       3460       3470       3480       3490       3500
TTAATCAGTG AGGCACCTAT CTCAGCGGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCCGCGGGG

3510       3520       3530       3540       3550       3560       3570
GGGCGGCTG  AGGTCTCGCCT CGTGAGAGAAG GTGTTGCTGA CTCATACCAG GCCTGAATCG CCCCATCATC

3580       3590       3600       3610       3620       3630       3640
CAGCCAGAAA GTGAGGGAGC CACGGTTGAT GAGAGCTTTG TTGTAGGTGG ACCAGTTGGT GATTTTGAAC

3650       3660       3670       3680       3690       3700       3710
TTTTGCTTTG CCACGGAAG  GTCTGCGTTG TCGGGAAGAT GGGTGATCTG ATCCTTCAAC TCAGCAAAAG

3720       3730       3740       3750       3760       3770       3780
TTCGATTTAT TCAACAAAGC CCCGTCCCG  TCAAGTCAGC GTAATCCTCT GCCAGTGTTA CAACCAATTA

3790       3800       3810       3820       3830       3840       3850
ACCAATTGTG ATTAGAAAAA CTCATCGAGC ATCAAATGAA ACTGCAATTT ATTCATATCA GGATTATCAA

3860       3870       3880       3890       3900       3910       3920
TACCATATTT TTGAAAAAGC CGTTTCTGTA ATGAGGAGA  AAACTCACCG AGGCAGTTCC ATAGGATGGC
```

FIG.6H

```
3930       3940       3950       3960       3970       3980       3990
AATATCCTTG TATCGGTCTG CGATTCCGAC TGGTCCAACA TCAATACAAC CTATTAATTT CCCCTCGTCA

4000       4010       4020       4030       4040       4050       4060
AAAATAAGGT TATCAAGTGA GAAATCACCA TGAGTGACGA CTGAATCCGG TGAGAATCGC AAAAGCTTAT

4070       4080       4090       4100       4110       4120       4130
GCATTCTTT  CCAGACTTGT TCAACAGGCC AGCCATTACG CTGTCATCA  AAATCACTCG CATCAACCAA

4140       4150       4160       4170       4180       4190       4200
ACGGTTATTC ATTCGTGATT GGGCCTGAGC GAGACGAAAT ACGGATGGC  TGTTAAAAG  ACAATTACAA

4210       4220       4230       4240       4250       4260       4270
ACAGGAATCG AATGCAACCG GGCCAGAAC  ACTGCCAGCG CATCAACAAT ATTTTCACCT GAATCAGGAT

4280       4290       4300       4310       4320       4330       4340
ATTCTTCTAA TACCTGGAAT GCTGTTTCC  CGGGATGGC  AGTGGTGAGT AACCATGCAT CATCAGGAGT

4350       4360       4370       4380       4390       4400       4410
ACGGATAAAA TGCTTGATGG TGGAAGAGG  CATAAAATCC GTCAGCCAGT TTAGTCTGAC CATTCATCT

4420       4430       4440       4450       4460       4470       4480
GTAACATCAT TGGCAACGCT ACCTTGCCA  TGTTTCAGAA ACAACTCTGG CGCATCGGGC TTCCCATACA
```

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FIG.6I

```
4490        4500        4510        4520        4530        4540        4550
ATGGATAGAT  TGTCGCACCT  GATTGCCGGA  CATTATCGGG  AGCCCATTTA  TACCATATATA AATCAGCATC

4560        4570        4580        4590        4600        4610        4620
CATGTTGGAA  TTTAATCGCG  GCCTCGAGCA  AGACGTTCC   CGTTGAATAT  GCCTCATAAC  GTTCCTTGTA

4630        4640        4650        4660        4670        4680        4690
TTACTGTTTA  TGTAAGCAGA  CAGTTTATT   GTTCATGATG  ATATATTTTT  ATCTTGTGCA  ATGTAACATC

4700        4710        4720        4730        4740        4750        4760
AGAGATTTTG  AGACACAACG  TGGCTTTCCC  CCCCCCCA    TTATTGAAGC  ATTTATCAGG  GTTATTGTCT

4770        4780        4790        4800        4810        4820        4830
CATGAGGGGA  TACATATTTG  AATGTATTTA  GAAAAATAAA  CAAATAGGGG  TTCGGGCAC   ATTTCCCGA

4840        4850        4860        4870        4880        4890        4900
AAAGTGCCAC  CTGAGCTCTA  AGAAACCATT  ATTATCATGA  CATTAACCTA  TAAAAATAGG  CGTATCACGA

4910
GGCCCTTTCG TC
```

FIG.7

```
          10          20          30          40          50          60          70
CTGCCAGTCAC CGTCGTTGAC CAGAGCTTGAG ATCCTACAGG AGTCCAGGC TGGAGAGAAA ACCTCTGCGA

          80          90          100         110         120         130         140
GGAAAGGGAA CGGAGCCAAGCC GTTGAATTTAA GGGACCCTGT GAAGCAAATCA TGGATGCAAT GAAGAGAGGG

          150         160         170         180
CTCTCGCTGTG TGCTTGCTGCT GTGTGGAGCA GTCTTGGTTT CGCCCAGC
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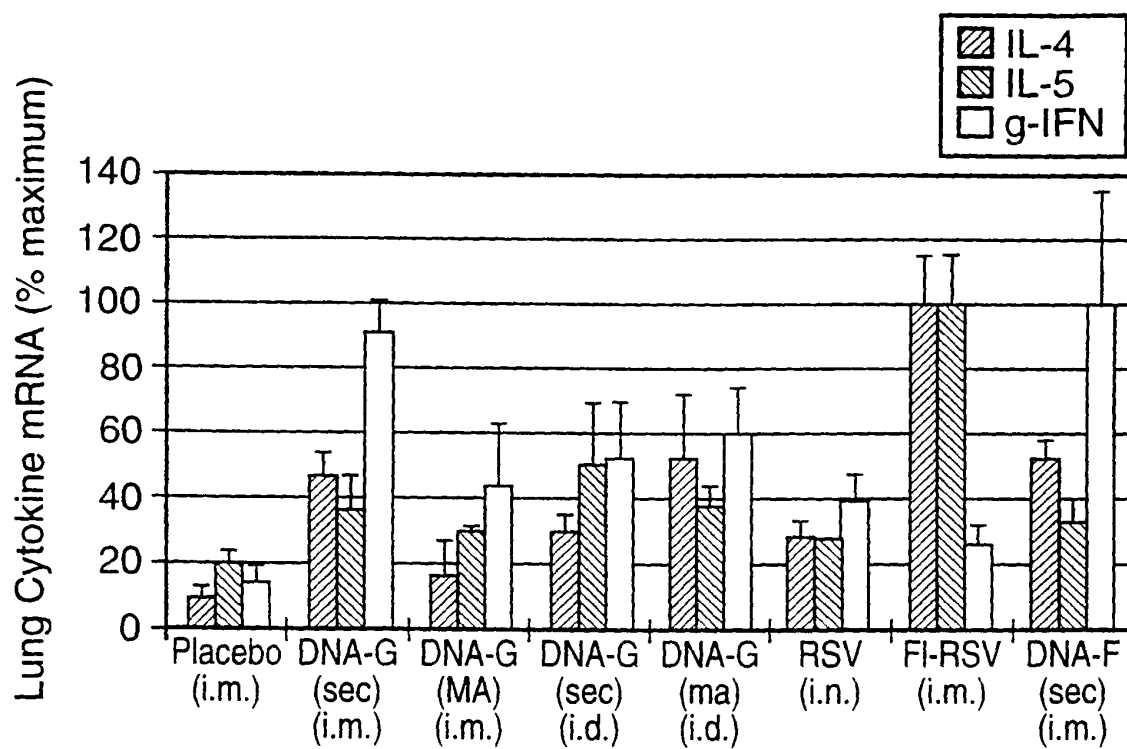
FIG.8